

# FIG. 1A

ctcgctccttcacttgataactgtggtaattctagagctaatacatgccgacggc 60  
gctgaccccccattcgggggggatgcgtgcatttatcagatcaagaccaaccggc 120  
cccttcggccccggccggggggcggcggcttggtactctagataaccc 180  
ggccgatcgacgccccctgtggcgacgacccattcgaacgtctgccctataact 240  
ttcgatggtagtcgcgtgcctaccatggtgaccacgggtgacggggatcagggttc 300  
ttccggagagggagcctgagaaacggctaccacatccaaggaaaggcagcaggcg 360  
ttacccactccggaggtggcgccatcttggcgaagggggatcaggaagtgcg 420  
gaccgcggcgccggcggcggcggcggcggcggcggcggcggcggcggcggaggc 480  
ccggccccggccccggagcggagcggagcggaggatgcagcagccgcagccgcagg 540  
cagcagcagccggggccggggcagcagctggggggcagggggcggcgcgggggggg 600  
ggcgccccagggggggggccggggccggggccctgcctgaggcgagagctgaagctg 660  
gagtccatcttccaccgcggccacgcgcgttccgcattgccagcgcctgcctggac 720  
ctgagctgcagttcctgctggctggccggagggccggggccggccggccgg 780  
ccgcacatccccccacgggggtcggtgcctgggatctgtccgcattccactgcaacatc 840  
acggagtcataccctgctgtgcggccatctggcgggtggagtcgtatgaccctaacttg 900  
gctgctgtcttggagaggctggacataaagaaaggaaatactctgtattgcagcat 960  
ctgaagaggatcatctccgaccctgtgtaaactctataaccctccctcagcatccagatgt 1020  
gagatgctggatcaacccttgccagcagcagtcgcacacaggaagacgtgtttcagaa 1080  
gatgaagatgaggagatgcctgaggacacagaagacttagatcactatgaaatgaaagag 1140  
gaagagccagctgaggcaagaaatctgaagatgatggcattggaaaagaaaacttggcc 1200  
atcctagagaaaattaaaaagaaccagaggcaagattacttaatggtcagtgatgttgc 1260  
tcggcaggccactgaccggctgtatggagctcaggatataccgatcacagagt 1320  
ttcaaaggcggaaactatgcagtcgaactcgtgaatgacagtctgtatgattggaaatgtc 1380  
aaactcctcaaagttgaccaggacagcgcttgcacaacgatctccagatcctcaaagag 1440

## FIG. 1B

aaagaaggagccgacttcattctacttaactttcctttaagataacttcccttgac 1500  
ccaccatttgtcagggttgtctccagtccctctggaggatgttctggcgagg 1560  
gccatctgcacggaaacttctcaccaaacagggtggagcgtgcctactccatagatca 1620  
gtgatcatgcagatcagtgcacactggtaagggaaagcacgagtcagttggagcc 1680  
aacaaatctaatacagtctgacaagagcacagcagtcctacaagtccctggatc 1740  
cacaaaaaaaacggctggtacacacccccaaaagaagacggctaaccctggagtatcacc 1800  
cttcctccctccccaggcaccactggaccaattaccttgaatgctgtatggatctca 1860  
cgctgcctctgtggccctccctcatttcctggacgtgatagctctgcctattgcag 1920  
gacaatgatggctattctaaacgctaaggaaaaaaaaacaaacacagaactgttcaagta 1980  
ctcaagactgacttacagaccaaccaaccacccctgctggAACCTGCTAGCAGGCATTc 2040  
ttataaaagaaactttcgagcctcattatgtctggaaactcagctgtgctccagacta 2100  
gaggcctccttacctatgctatggatTTTAATTtATTTCTTATTCTGTACACTGC 2160  
ttttttggttacagtgtatgtatggatgttatgaaaaaaatgtatcttggaaaacaa 2220  
ttacagttgttaattgaaaaaaaaaaaaaaaaa 2280

(SEQ ID NO:1)

## FIG. 2A

CTCGCTCCTCTCCTACTTGGATAACTGTGGTAATTCTAGAGCTAACATGCCGACGGGC  
GCTGACCCCCCTTCGGGGGGGGATGCGTGCAATTATCAGATCAAGACCAACCCGGTCAGC  
CCCTCTCCGGCCCCGGGGGGGGCGGGCGCCGGCGGGCTTGGGTGACTCTAGATAACCTC  
GGCCGATCGCACGCCCCCGTGGCGCGACGACCCATTGAACGTCTGCCCTATCAACT  
TTCGATGGTAGTCGCCGTGCTACCATGGTGACCACGGGTGACGGGAATCAGGGTTCGA  
TTCCGGAGAGGGAGGCCTGAGAAACGGCTACCAAGGAAGGCAGCAGGGCGCGAAA  
TTACCCACTCCCGAGGTGGCGCGGCCATCTTGGCGAAGGGGGATCAGGAAGTGCG  
GACCGCGGCGGCGCGCGCGCGCGCGAGCCGGAGGCCAGGCCAGGCCAGGCCAGGG  
CGGGCCCGCCGGCCCCGGAGCGGAGCGGAGGGATGCAGCAGCCGAGCCGAGGG  
M Q Q P Q P Q G  
CAGCAGCAGCCGGGGCCGGGGCAGCAGCTGGGGGGCCAGGGGGCGCCGGGGGGCGGG  
Q Q Q P G P G Q Q L G G G Q G A A P G A G  
GGCGGCCAGGGGGGGCCCGGGGGCCCTGCCTGAGGCGAGAGCTGAAGCTGCTC  
G G P G G G P G P C L R R E L K L L  
GAGTCCATCTTCCACCGCGGCCACGAGCGCTCCGCATTGCCAGGCCCTGCCAGAG  
E S I F H R G H E R F R I A S A C L D E  
CTGAGCTGAGTTCTGCTGGCTGGGGCCGGAGGGGGCCGGGGGGCCGCCGGGG  
L S C E F L L A G A G G A G A G A A P G  
CCGCATCTCCCCCAGGGGGCTGGTGCTGGGATCCTGTCCGCATCCACTGCAACATC  
P H L P P R G S V P G D P V R I H C N I  
ACGGAGTCATACCCCTGCTGTGCCCCCCCATCTGGTCGGTGGAGTCTGATGACCTAACTTG  
T E S Y P A V P P I W S V E S D D P N L  
GCTGCTGTCTTGGAGAGGCTGGTGGACATAAAGAAAGGAAATACTCTGCTATTGCAGCAT  
A A V L E R L V D I K K G N T L L L Q H  
CTGAAGAGGATCATCTCCGACCTGTGAAACTCTATAACCTCCCTCAGCATCCAGATGTG  
L K R I I S D L C K L Y N L P Q H P D V  
GAGATGCTGGATCAACCTTGCCAGCAGAGCAGTGCACACAGGAAGACGTGCTTCAGAA  
E M L D Q P L P A E Q C T Q E D V S S E  
GATGAAGATGAGGAGATGCCCTGAGGACACAGAACAGACTTAGATCACTATGAAATGAAAGAG  
D E D E E M P E D T E D L D H Y E M K E  
GAAGAGCCAGCTGAGGGCAAGAAATCTGAAGATGATGGCATTGGAAAAGAAAACCTGGCC  
E E P A E G K K S E D D G I G K E N L A  
ATCCTAGAGAAAATTAAAAAGAACCAAGAGCAAGATTACTTAAATGGTGCAGTGTCTGGC  
I L E K I K K N Q R Q D Y L N G A V S G  
TCGGTGCAGGCCACTGACCGGCTGATGAAGAGCTCAGGGATATACCGATCACAGAGT  
S V Q A T D R L M K E L R D I Y R S Q S  
TTCAAAGGCGGAAACTATGCAGTCGAACCTCGTGAATGACAGTCTGTATGATTGGAATGTC  
F K G G N Y A V E L V N D S L Y D W N V  
AAACTCCTCAAAGTTGACCAAGGACAGCGCTTGACAAACGATCTCCAGATCCTCAAAGAG  
K L L K V D Q D S A L H N D L Q I L K E  
AAAGAAGGAGGCCACTTCATTCTACTTAACTTTCTTAAAGATAACTTCCCTTGAC  
K E G A D F I L L N F S F K D N F P F D  
CCACCATTGTCAGGGTTGTCTCCAGTCCTCTGGAGGGTATGTTCTGGCGGGAGGG  
P P F V R V V S P V L S G G Y V L G G G  
GCCATCTGCATGGAACCTCTCACCAAACAGGGCTGGAGCAGTGCCTACTCCATAGAGTCA  
A I C M E L L T K Q G W S S A Y S I E S  
GTGATCATGCAGATCAGTGCCACACTGGTGAAGGGAAAGCACGAGTGCAGTTGGAGCC  
V I M Q I S A T L V K G K A R V Q F G A

## FIG. 2B

AACAAATCTCAATACTAGTCTGACAAGAGCACAGCAGTCCTACAAGTCCTGGTGCAGATC  
N K S Q Y S L T R A Q Q S Y K S L V Q I  
CACGAAAAAAACGGCTGGTACACACCCCCAAAAGAAGACGGCTAACCTGGAGTATCACC  
H E K N G W Y T P P K E D G \*  
CTTCCTCCCTCCCCAGGCACCACTGGACCAATTACCTTGAATGCTGTATTTGGATCTCA  
CGCTGCCTCTGTGGTCCCTCCCTCATTTCTGGACGTGATAGCTCTGCCTATTGCAG  
GACAATGATGGCTATTCTAACGCTAAGGAAAAAAACAAACACAGAACTGTTCAAGTA  
CTCAAGACTGACTTACAGACCAACCAACCACCTTGCTGGAACCCCTGCTAGCAGGCATTC  
TTATAAAAGAAACTTTCGAGCCTCTTATATTGCTGGAAACTCAGCTGTGCTCCAGACTA  
GAGCCTCCTTACCTATGCTATGGATTTAATTCTTCTTATTCATGTACACTGC  
TTTTTTGGTTACAGTGTATGGATGTGTGAAAGAAATGTATCTTGGAAAACAA  
TTACAGTTGTTAATTGAAAAA

FIG. 3

MQQPQPQGQQ	QPGPGQQQLGG	QGAAPGAGGG	PGGGPGPGPC	40
LRRELKLLES	IFHRGHERFR	IASACLDELS	CEFLLAGAGG	80
AGAGAAPGPH	LPPRGSVPGD	PVRIHCNITE	SYPAVPPIWS	120
VESDDPNLAA	VLERLVDIKK	GNTLLLQHLK	RIISDLCKLY	160
NLPQHPDVEM	LDQPLPAEQC	TQEDVSSEDE	DEEMPEDTED	200
LDHYEMKEEE	PAEGKKSEDD	GIGKENLAIL	EKIKKNQRQD	240
YLNGAVSGSV	QATDRLMKEL	RDIYRSQSFK	GGNYAVELVN	280
DSLYDWNVKL	LKVDQDSALH	NDLQILKEKE	GADFILLNFS	320
FKDNPPFDPP	FVRVVSPVLS	GGYVLGGGAI	CMELLTKQGW	360
SSAYSIESVI	MQISATLVKG	KARVQFGANK	SQYSLTRAQQ	400
SYKSLVQIHE	KNGWYTPPK	DG		422
(SEQ ID NO:2)				

(SEQ ID NO:2)

FIG. 4

65

RATL1d6	(1)	MQQPQPQQPGPGQQLGGQAAAPGAGGGPGGGPGPGPCLRRELKLLSIFHRGHERFRIASAC
T21349_F25H2.8_Cel	(1)	-----MACLRKLKEDIQVLEKLFPKNHNRFQILSSA
AAF45767_EG:25E8_Dr	(1)	-----MACLNTLKQEIKTLEKIFPKNHERFQILNSS

66

RATL1d6	(66)	LDELSCEFLLAGAGGAGAGAAPGPHLPPRGSPVGDPVRICHNCITESYPAVPPIVSVESSDDPNLAA
T21349_F25H2.8_Cel	(32)	VDELMSMKFINAEN-----KG-----IIVTANIQENYPRQPPIWFSSESDDVPVIG
AAF45767_EG:25E8_Dr	(32)	VDELLCRFIDKNG-----KR-----YDIHANITETYPSSPPWFAESEETSVTN

130

131

RATL1d6	(131)	VLERLVDIKKGNLQLHLKRISDLCKLYNLQHPDVEMLDQPL-----
T21349_F25H2.8_Cel	(76)	MSLQRLTETEESTNILHQVHRLVSDLCSFYNLQMPCELPQIAPPVRDD-----IDEGRGSDI
AAF45767_EG:25E8_Dr	(76)	AVQILSNTNGRDNHVINQVGILLRECLRLHNVPPLPDIDNLALPLQTTPPSASPLRCEQRPGGGG

195

196

RATL1d6	(176)	-----PAEQCTQEDVSSEDEDEEMPEDTEDLDHYEMKEEPAEGKKSEDDGIGKENLAILEKIK
T21349_F25H2.8_Cel	(133)	SDTTSEPIDDDMAGDGEVDDDEEEEDDEDADGDIEIVEMAEEDPTSQHDVGVSKEGLDMUDKVS
AAF45767_EG:25E8_Dr	(141)	AGGGGGPHGNEETDSDQEEIEDPIGESEQESEGDEDLPLEMDVRSSTSKKDDMEVEHLATLEKLR
P52483_UB6B_MOUSE	(1)	-----MSSDRQRSDDESPSTSSGSSADQRDP

260

261

RATL1d6	(235)	KNQRQDYLNQAVSGSVQATDRIMKELRDIYRSQSFKGGNYAVELVN-DSLYDWNVKILKVDQSA
T21349_F25H2.8_Cel	(198)	KINRQHQHLDGKVQGSITATDRIMKEIRDIHRSFHKNGIYTFELEKEENLYQOWWIKILHKVDBDSP
AAF45767_EG:25E8_Dr	(206)	QSQRQDYLKGGSVSGSVQATDRIMKELRDIYRSDAFKKNMYSIELVN-ESIYEWNRILKSVDPDSP
P52483_UB6B_MOUSE	(28)	AAPKPEEQERKPSATQQKKNTKLSSKTTAKLSTSAAKRIQKELAEITLDPPPNCAGPKCDNIYE
P27924_UBC1_HUMAN	(1)	-----MANIAVQRIKREFKEVLKSEETSKNQIKVLDLV-----ENFT-E
CAA72184_UBCD4_Dr	(1)	-----MANMAVSRRIKREFKEVMRSSEEIVQCSIKELVN-----DSWTE
P14682_UBC3_YEAST	(1)	-----MSSRKSTASSLLRQYRELTDPKKAIPSFHIELEDD-----SNIFTW

325

326

RATL1d6	(299)	LHNDLQILKEKEGA-DFILLNESHKDNFEPDPPFVRRVSPVLSGGYVLGGGAICMELLTKQG-----
T21349_F25H2.8_Cel	(263)	LFEDDMKKLKKDHNO-DHLLFSFTIPEKFECPPFVRRVAPHINQGFVLGGGAICMELLTKQG-----
AAF45767_EG:25E8_Dr	(270)	LHSDLQMLKEKEGK-DSILLNLFKETYPFEPPFVRRVPHPIISGGYVLIGGAIICMELLTKQG-----
P52483_UB6B_MOUSE	(93)	WRSTILLGPEGSVYEGGVFFLDITHESSDYPKPPKVTTERTRIYHCNINSQ-GVICLDDILKD-----
P27924_UBC1_HUMAN	(39)	LRGEIAGPPDTPYEGGRYQLEIKIPETYPFPNPPKVRFTTIWHPNISSVTGAIICLDDILKD-----
CAA72184_UBCD4_Dr	(39)	LRGEIAGPPDTPYEGGKFVLEIKVPETYPFPNPPKVRFTTRIWHPNIISVTGAIICLDDILKD-----
P14682_UBC3_YEAST	(43)	NICGMVLNEDSIYHGCFFKAQMRFPEDFPESPPQFRRTPAIVHPNVYRD-GRLCISILHQSGDPM

390

391

RATL1d6	(360)	-----WSSAYSIESVIMQISATLVKGKARVQFGANK-----SQYSLTRAQQSYKSLVQI
T21349_F25H2.8_Cel	(324)	-----WSSAYSIESCILQIAATLVKGKARISFDAKHT-----STYSMARAQQSFKSLVQI
AAF45767_EG:25E8_Dr	(331)	-----WSSAYTVEAVIMQIAATLVKGKARIQFGATKALTQ-----GQYSLARAQQSFKSLVQI
P52483_UB6B_MOUSE	(153)	-----WSPALTISKVLLSICSLLTDCNPADPLVGSIAT-----QYLTLRAEHDRARIQWT
P27924_UBC1_HUMAN	(100)	-----WAAAMTLRTVLLSLQALLAAAEPDDPODAVVAN-----QYKQNPEMFQQTARLWA
CAA72184_UBCD4_Dr	(100)	-----WAAAMTLRTVLLSLQALLAAAEPDDPODAVVAY-----QFKDKYDLFLTAKHWT
P14682_UBC3_YEAST	(107)	TDEPDAETWSPVQIVESVLIISIVSLLEDPNINSPANVDAAVDYRKNPEQYKQRVKMEVERSQDI

455

456

RATL1d6	(409)	HEKNGWYTPPKEDG-----
T21349_F25H2.8_Cel	(374)	HAKSGCTFLCSTPSSHFFALHLVFFLHSDDFFNGFLKSETFTFFKLSFRGYISSLVLYFSRHL
AAF45767_EG:25E8_Dr	(384)	HEKNGWFTTPPKEDG-----
P52483_UB6B_MOUSE	(203)	KRYAT-----
P27924_UBC1_HUMAN	(150)	FVYAGAPVSSPEYTKKIENLCAMGFDRNAVALSSKSWDVETATELLLSN-----
CAA72184_UBCD4_Dr	(150)	NAYAGGPHTFPDCDSKIQRLRDMGIDEHEARAVLSKENWNLEKATEGLFS-----
P14682_UBC3_YEAST	(172)	PKGFIMPTSESAYISQSKLDEPESNKDMADNFWYDSLDDDENGSVILQDDDYDDGNNHIFPFEDD

520

521

T21349_F25H2.8_Cel	(439)	HHPFTRFLIPQLQPPPPIPQLIPPFLNRTKHV-----
P14682_UBC3_YEAST	(237)	DVYNYNNDNDDDERIEFEDDDDDDDSIDNDSVMDRKQPHKAEDESEDVEDVERVSKKI

579

# FIG. 5A

RATL1d6 BLAST results/alignment w/ Drosophila protein

>GCGPROT:O46068 EG:25E8.2 PROTEIN.  
Length = 394  
Score = 369 bits (936), Expect = e-101  
Identities = 194/403 (48%), Positives = 265/403 (65%), Gaps = 51/403 (12%)  
  
Query: 41 LRRELKLLESIFHRGHERFRIASACLDELSCEFLLAGAGGGAGAGAAPGPHLPPRGSVPGD 100  
L++E+E K LE IF + HERF+I ++ +DEL C F+ G  
Sbjct: 7 LKQEIKTLEKIFPKNHERFQILNSSVDELLCRFI-----DKNGK 45  
  
Query: 101 PVRICHNITESYPAVPPIWSVESDDPNLAAVLERLVDIKKGNTLLLQHLKRIISDLCKLY 160  
IH NITE+YP+ PP+W ES++ ++ ++ L + + + + + + +LC+L+  
Sbjct: 46 RYDIHANITETYPSSPPVWFAESEETSVTNAVQILSNTNGRDNHVINQVGILLRELCRLH 105  
  
Query: 161 NLPQHPDVEMLDQPLPAEQCTQEDVSSEDE-----DEEMPEDTEDLDHYEM 206  
N+P PD++ L PL + + E +EE D E+++  
Sbjct: 106 NVPLPPDIDNLALPLQTTPPSASPLRCEQRPGGGAGGGGGPHGNEETSDQEEIEDPIG 165  
  
Query: 207 KEEEPAAEGKK-----SEDDGIGKENLAILEKIKKNQRQDYLNQAVSGSVQATD 254  
+ E+ +EG + S+ D + E+LA LEK+++QRQDYL G+VSGSVQATD  
Sbjct: 166 ESEQESEGDEDLPLEMDDRSTSQQDDMEVEHLATLEKLRQSQRQDYLKGSVSGSVQATD 225  
  
Query: 255 RLMKELRDIYRSQSFKGNNYAVELVNDSL YDWNVKLLKVDQDSALHNDLQILKEKEGADF 314  
RLMKELRDIYRS +FK Y++ELVN+S+Y+WN++L VD DS LH+DLQ+LKEKEG D  
Sbjct: 226 RLMKELRDIYRSDAFKKNMYSIELVNESIYEWNLKSVDPSPLHSDLQMLKEKEGKDS 285  
  
Query: 315 ILLNFSFKDNFPFDPPFVRRVSPVLGGYVLGGGAICMELLTKQGWSSAYSIESVIMQIS 374  
ILLN FK+ +PF+PPFVRRV P++SGGYVL GGAICMELLTKQGWSSAY++E+VIMQI+  
Sbjct: 286 ILLNILFKETYPPFEPPFVRRVHPIISGGYVLIGGAICMELLTKQGWSSAYTVEAVIMQIA 345  
  
Query: 375 ATLVKKGKARVQFGANKS---QYSLTRAQQSYKSLVQIHEKNG 413  
ATLVKGKAR+QFGA K+ QYSL RAQQS+KSLVQIHEKNG  
Sbjct: 346 ATLVKKGKARIQFGATKALTQGQYSLARAQQSFKSLVQIHEKNG 388

## FIG. 5B

RATL1d6 BLAST results/alignment w/ C. elegans protein

>GCGPROT:Q93571 F25H2.8 PROTEIN.  
Length = 471  
Score = 317 bits (805), Expect = 6e-86  
Identities = 178/397 (44%), Positives = 247/397 (61%), Gaps = 49/397 (12%)  
  
Query: 41 LRRELKLLESIFHRGHFERFRIASACLDELSCEFLLAGAGGAGAGAAPGPHLPPRGSVPGD 100  
L+ +++LE +F + H RF+I SA +DELS +F+ A G  
Sbjct: 7 LKEDIQVLEKLFPKNHNRFQILSASVDELSMKFINAENKG----- 46  
  
Query: 101 PVRIHCNITESYPAVPPIWSVESDD-PNLAAVLERLVDIKKGNTLLLQHLKRIISDLCKL 159  
+ + NI E+YP PPIW ESDD P + L+RL + ++ +T +L + R++SDLC  
Sbjct: 47 -IIVTANIQENYPRQPPWFSESDDPVIGMSILQRLTETEE-STNILHQVHRLVSDLCSF 104  
  
Query: 160 YNL-----PQHPDVE-----MLDQPLPAEQCTQEDVSSEDEDEEMPEDTE 199  
YNL P D++ +P+ + +V +DE+EE ED +  
Sbjct: 105 YNLQMPCELPQIAPPVRDDIDEGRGSDISDTSEPIDDDMAGDGEVDDDDEEEEDDEDAD 164  
  
Query: 200 -DLDHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQATDRLMK 258  
D++ EM EE+P D G+ KE L +L+K+ K RQ +L+G V GS+ ATDRLMK  
Sbjct: 165 GDIEIVEMAEEDPTS---QHDVGVSKEGLDMILDKVSKINRQQHLDGKVQGSITATDRLMK 221  
  
Query: 259 ELRDIYRSQSFKGNYAVELVND-SLYDWNVKLLKVDQDSALHNDLQILKEKEGADFILL 317  
E+RDI+RS+ FK G Y EL + +LY W +KL KVD+DS L D++ LK+ D +L  
Sbjct: 222 EIRDIHRSEHFKNGIYTFELEKEENLYQWWIKLHKVDEDSPFEDMKLKKDHNQDHLLF 281  
  
Query: 318 NFSFKDNFPFDPPFVRVVSPVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQISATL 377  
+F+F + FP DPPFVRVV+P ++ G+VLGGGAICMELLTKQGWSSAYSIES I+QI+ATL  
Sbjct: 282 SFTFNEKFPCDPPFVRVVAPHINQGFVLGGGAICMELLTKQGWSSAYSIESCILQIAATL 341  
  
Query: 378 VKGKARVQFGA-NKSQYSLTRAQQSYKSLVQIHEKNG 413  
VKG+AR+ F A + S YS+ RAQOS+KSL QIH K+G  
Sbjct: 342 VKGRARISFDAKHTSTYSMARAQQSFKSLQQIHAKSG 378

**FIG. 6**

